



B1

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Betzner, Andreas
Freyssinet, Georges
Perez, Pascal

<120> METHOD FOR OBTAINING PLANT VARIETIES

<130> A33153-PCT-USA 072667.0128

<140> US 09/529,239

<141> 2000-10-27

<150> PCT/EP98/06977

<151> 1998-10-09

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<220>
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ecotype Columbia

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Pro Pro Pro Lys Ile Ser Ala Thr Val Ser Phe Ser Pro Ser Lys Arg	
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Lys Leu Leu Ser Asp His Leu Ala Ala Ser Pro Lys Lys Pro Lys	
50 55 60	
ctt tct cct cac act caa aac cca gta ccc gat ccc aat tta cac caa	339
Leu Ser Pro His Thr Gln Asn Pro Val Pro Asp Pro Asn Leu His Gln	
65 70 75 80	
aga ttt ctc cag aga ttt ctg gaa ccc tcg ccg gag gaa tat gtt ccc	387
Arg Phe Leu Gln Arg Phe Leu Glu Pro Ser Pro Glu Glu Tyr Val Pro	
85 90 95	
gaa acg tca tca tcg agg aaa tac aca cca ttg gaa cag caa gtg gtg	435
Glu Thr Ser Ser Ser Arg Lys Tyr Thr Pro Leu Glu Gln Val Val	
100 105 110	
gag cta aag agc aag tac cca gat gtg gtt ttg atg gtg gaa gtt ggt	483
Glu Leu Lys Ser Lys Tyr Pro Asp Val Val Leu Met Val Glu Val Gly	
115 120 125	
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Pro Thr Phe Arg Leu Asn Phe His Val Arg Arg Leu Val Asn Ala Gly	
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His Gly Ala Asn Arg Thr Gly Pro Phe Phe Arg Gly Leu Ser Ala Leu	
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Tyr Thr Lys Ala Thr Leu Glu Ala Ala Glu Asp Ile Ser Gly Gly Cys	
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225 230 235 240	
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Ser Phe Asp Val Arg Val Gly Val Val Gly Val Glu Ile Ser Thr Gly	
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Gly Asn Leu Glu Asp Asp Lys Glu Met Lys Leu Glu Ala Ala Glu Lys	
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Gly Met Ser Cys Leu Thr Val His Thr Ile Met Asn Met Pro His Leu	
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Pro Glu Phe Tyr Leu Val Leu Ser Ser Val Leu Thr Ala Met Ser Arg	
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Ser Ser Asp Ile Gln Arg Gly Ile Thr Arg Ile Phe His Arg Thr Ala	
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Lys Ala Thr Glu Phe Ile Ala Val Met Glu Ala Ile Leu Leu Ala Gly	
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625 630 635 640	
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Thr His Leu Ile Glu Leu Pro Val Asp Ser Lys Val Pro His Asn Trp	
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Val Lys Val Asn Ser Thr Lys Lys Thr Ile Arg Tyr His Pro Pro Glu	
690 695 700	
ata gta gct ggc ttg gat gag cta gct cta gca act gaa cat ctt gcc	2259
Ile Val Ala Gly Leu Asp Glu Leu Ala Leu Ala Thr Glu His Leu Ala	
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725 730 735	

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Cys Leu His Ser Leu Ser Thr Leu Ser Arg Asn Lys Asn Tyr Val Arg	
755 760 765	
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Pro Glu Phe Val Asp Asp Cys Glu Pro Val Glu Ile Asn Ile Gln Ser	
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Gly Arg His Pro Val Leu Glu Thr Ile Leu Gln Asp Asn Phe Val Pro	
785 790 795 800	
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Ile Ser Ile Met Ala Gln Val Gly Ser Phe Val Pro Ala Ser Phe Ala	
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Lys Leu His Val Leu Asp Gly Val Phe Thr Arg Met Gly Ala Ser Asp	
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Ser Ile Gln His Gly Arg Ser Thr Phe Leu Glu Glu Leu Ser Glu Ala	
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Ser His Ile Ile Arg Thr Cys Ser Ser Arg Ser Leu Val Ile Leu Asp	
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Glu Leu Gly Arg Gly Thr Ser Thr His Asp Gly Val Ala Ile Ala Tyr	
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Ala Thr Leu Gln His Leu Leu Ala Glu Lys Arg Cys Leu Val Leu Phe	
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Val Thr His Tyr Pro Glu Ile Ala Glu Ile Ser Asn Gly Phe Pro Gly	
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Gly Ser Tyr Asp His Asp Asp Val Thr Tyr Leu Tyr Lys Leu Val Arg	
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 Glu Ala Glu Val Arg Ala Arg Glu Arg Asn Thr Arg Met Gly Glu Pro
 1010 1015 1020
 gaa gga cat gaa gaa ccg aga ggc gca gaa gaa tct att tcg gct cta 3219
 Glu Gly His Glu Glu Pro Arg Gly Ala Glu Glu Ser Ile Ser Ala Leu
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 ggt gac ttg ttt gca gac ctg aaa ttt gct ctc tct gaa gag gac cct 3267
 Gly Asp Leu Phe Ala Asp Leu Lys Phe Ala Leu Ser Glu Glu Asp Pro
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 tgg aaa gca ttc gag ttt tta aag cat gct tgg aag att gct ggc aaa 3315
 Trp Lys Ala Phe Glu Phe Leu Lys His Ala Trp Lys Ile Ala Gly Lys
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 atc aga cta aaa cca act tgt tca ttt tgatttaatc ttaacattat 3362
 Ile Arg Leu Lys Pro Thr Cys Ser Phe
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 <212> PRT
 <213> Arabidopsis thaliana ecotype Columbia
 <223> Polypeptide MSH3

<400> 19

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 35 40 45
 Lys Leu Leu Ser Asp His Leu Ala Ala Ala Ser Pro Lys Lys Pro Lys
 50 55 60
 Leu Ser Pro His Thr Gln Asn Pro Val Pro Asp Pro Asn Leu His Gln
 65 70 75 80
 Arg Phe Leu Gln Arg Phe Leu Glu Pro Ser Pro Glu Glu Tyr Val Pro
 85 90 95
 Glu Thr Ser Ser Ser Arg Lys Tyr Thr Pro Leu Glu Gln Gln Val Val

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Pro	Thr	Phe	Arg	Leu	Asn	Phe	His	Val	Arg	Arg	Leu	Val	Asn	Ala	Gly
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His	Gly	Ala	Asn	Arg	Thr	Gly	Pro	Phe	Phe	Arg	Gly	Leu	Ser	Ala	Leu
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Thr	Ser	Asn	Val	Arg	Val	Glu	Arg	Ala	Ser	Leu	Asp	Cys	Phe	Ser	Asn
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Phe	Glu	Arg	Ile	Leu	Tyr	Gln	Gly	Ala	Ser	Phe	Arg	Ser	Leu	Ser	Ser
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420										425					430						
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		435					440					445									
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	450					455					460										
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Ala	Val	Ser	Glu	Ile	Ser	Ala	Cys	Met	Gly	Ser	His	Ser	Ser	Ser	Gln						
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Leu	Ser	Ser	Glu	Leu	Val	Glu	Glu	Gly	Ser	Glu	Arg	Ala	Ile	Val	Ser						
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Pro	Glu	Phe	Tyr	Leu	Val	Leu	Ser	Ser	Val	Leu	Thr	Ala	Met	Ser	Arg						
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Lys	Ala	Thr	Glu	Phe	Ile	Ala	Val	Met	Glu	Ala	Ile	Leu	Leu	Ala	Gly						
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Lys	Gln	Ile	Gln	Arg	Leu	Gly	Ile	Lys	Gln	Asp	Ser	Glu	Met	Arg	Ser						
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Met	Gln	Ser	Ala	Thr	Val	Arg	Ser	Thr	Leu	Leu	Arg	Lys	Leu	Ile	Ser						
			580					585					590								
Val	Ile	Ser	Ser	Pro	Val	Val	Val	Asp	Asn	Ala	Gly	Lys	Leu	Leu	Ser						
		595					600					605									
Ala	Leu	Asn	Lys	Glu	Ala	Ala	Val	Arg	Gly	Asp	Leu	Leu	Asp	Ile	Leu						
	610					615					620										
Ile	Thr	Ser	Ser	Asp	Gln	Phe	Pro	Glu	Leu	Ala	Glu	Ala	Arg	Gln	Ala						
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Val	Leu	Val	Ile	Arg	Glu	Lys	Leu	Asp	Ser	Ser	Ile	Ala	Ser	Phe	Arg						
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Thr	His	Leu	Ile	Glu	Leu	Pro	Val	Asp	Ser	Lys	Val	Pro	His	Asn	Trp						
		675					680						685								
Val	Lys	Val	Asn	Ser	Thr	Lys	Lys	Thr	Ile	Arg	Tyr	His	Pro	Pro	Glu						
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Ile	Val	Ala	Gly	Leu	Asp	Glu	Leu	Ala	Leu	Ala	Thr	Glu	His	Leu	Ala						
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Ile	Val	Asn	Arg	Ala	Ser	Trp	Asp	Ser	Phe	Leu	Lys	Ser	Phe	Ser	Arg						
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Cys	Leu	His	Ser	Leu	Ser	Thr	Leu	Ser	Arg	Asn	Lys	Asn	Tyr	Val	Arg
	755						760					765			
Pro	Glu	Phe	Val	Asp	Asp	Cys	Glu	Pro	Val	Glu	Ile	Asn	Ile	Gln	Ser
	770					775					780				
Gly	Arg	His	Pro	Val	Leu	Glu	Thr	Ile	Leu	Gln	Asp	Asn	Phe	Val	Pro
785					790					795					800
Asn	Asp	Thr	Ile	Leu	His	Ala	Glu	Gly	Glu	Tyr	Cys	Gln	Ile	Ile	Thr
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			820					825					830		
Ile	Ser	Ile	Met	Ala	Gln	Val	Gly	Ser	Phe	Val	Pro	Ala	Ser	Phe	Ala
		835					840				845				
Lys	Leu	His	Val	Leu	Asp	Gly	Val	Phe	Thr	Arg	Met	Gly	Ala	Ser	Asp
	850					855					860				
Ser	Ile	Gln	His	Gly	Arg	Ser	Thr	Phe	Leu	Glu	Glu	Leu	Ser	Glu	Ala
865						870				875				880	
Ser	His	Ile	Ile	Arg	Thr	Cys	Ser	Ser	Arg	Ser	Leu	Val	Ile	Leu	Asp
				885					890					895	
Glu	Leu	Gly	Arg	Gly	Thr	Ser	Thr	His	Asp	Gly	Val	Ala	Ile	Ala	Tyr
			900					905					910		
Ala	Thr	Leu	Gln	His	Leu	Leu	Ala	Glu	Lys	Arg	Cys	Leu	Val	Leu	Phe
		915					920					925			
Val	Thr	His	Tyr	Pro	Glu	Ile	Ala	Glu	Ile	Ser	Asn	Gly	Phe	Pro	Gly
	930					935					940				
Ser	Val	Gly	Thr	Tyr	His	Val	Ser	Tyr	Leu	Thr	Leu	Gln	Lys	Asp	Lys
945						950				955				960	
Gly	Ser	Tyr	Asp	His	Asp	Asp	Val	Thr	Tyr	Leu	Tyr	Lys	Leu	Val	Arg
				965					970					975	
Gly	Leu	Cys	Ser	Arg	Ser	Phe	Gly	Phe	Lys	Val	Ala	Gln	Leu	Ala	Gln
			980				985					990			
Ile	Pro	Pro	Ser	Cys	Ile	Arg	Arg	Ala	Ile	Ser	Met	Ala	Ala	Lys	Leu
		995					1000					1005			
Glu	Ala	Glu	Val	Arg	Ala	Arg	Glu	Arg	Asn	Thr	Arg	Met	Gly	Glu	Pro
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Glu	Gly	His	Glu	Glu	Pro	Arg	Gly	Ala	Glu	Glu	Ser	Ile	Ser	Ala	Leu
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Gly	Asp	Leu	Phe	Ala	Asp	Leu	Lys	Phe	Ala	Leu	Ser	Glu	Glu	Asp	Pro
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Trp	Lys	Ala	Phe	Glu	Phe	Leu	Lys	His	Ala	Trp	Lys	Ile	Ala	Gly	Lys

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<210> 20
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> MSH6 specific primer 638 for PCR using cDNA of Arabidopsis thaliana ecotype Columbia

<400> 20

tctctaccag gtgacgaaaa accg 24

<210> 21
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Primer S81 for PCR using cDNA of Arabidopsis thaliana ecotype Columbia

<400> 21

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<210> 22
<211> 30
<212> DNA
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<220>
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<400> 22

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<210> 23
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<220>
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<400> 23

gacagcgtca gttcttcaga atgc 24

<210> 24
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 <212> DNA
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<220>
 <223> MSH6 specific primer 1S8 for PCR using cDNA of Arabidopsis thaliana ecotype Columbia

<400> 24

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<210> 25
 <211> 27
 <212> DNA
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<220>
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<400> 25

cgctatctat ggctgcttcg aattgag 27

<210> 26
 <211> 1385
 <212> DNA
 <213> Arabidopsis thaliana ecotype Columbia
 <223> Clone 43

<400> 26

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tctgtcgatg	aggtttagag	aacggatact	ccaccggaga	aggttccgcg	tcgtgtcctg	240
ccgtctggat	ttaagccggc	tgaatccgcc	ggtgatgctt	cgtccctgtt	ctccaatatt	300
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gttgttccgc	tgaatgattc	atctctatgt	atgaaggcta	atgatgttat	tcctcaattt	420
cgttccaata	atggtaaaac	tcaagaaaaga	aaccatgctt	ttagtttcag	tgggagagct	480
gaacttagat	cagtagaaga	tataggagta	gatggcgatg	ttcctgggtc	agaaacacca	540
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ttcagaagtg	gaattgatct	gttgttggct	ctacagaagg	aatcaaatac	gatgagtttg	2100
ctttataaac	tctgtaaact	tcctatatta	gtaggaaaaa	gcgggctaga	gttatttctt	2160
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 <211> 1385
 <212> DNA
 <213> Arabidopsis thaliana ecotype Columbia
 <223> Clone 62

<400> 27

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aaaacttcaa	gtcaagttag	ctaagatctg	agttctcaag	tctgcatgaa	gactggctca	1260
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ccggg					1385	

<210> 28
 <211> 34
 <212> DNA
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<220>
 <223> MSH6 specific primer 2S8 for PCR using cDNA of Arabidopsis thaliana ecotype Columbia

<400> 26

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<210> 29
<211> 27
<212> DNA
<213> Artificial sequence

<220>
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<400> 29

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<210> 30
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<220>
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<223> AtMSH6 full-length cDNA and deduced sequence of the encoded polypeptide

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tctctctcac aattccaaaa a atg cag cgc cag aga tcg att ttg tct ttc 171
Met Gln Arg Gln Arg Ser Ile Leu Ser Phe
1 5 10

ttc caa aaa ccc acc gcg gcg act acg aag ggt ttg gtt tcc ggc gat 219
Phe Gln Lys Pro Thr Ala Ala Thr Thr Lys Gly Leu Val Ser Gly Asp
15 20 25

gct gct agc ggc ggc ggc ggc agc gga gga cca cga ttt aat gtg aag 267
Ala Ala Ser Gly Gly Gly Gly Ser Gly Gly Pro Arg Phe Asn Val Arg
30 35 40

gaa ggc gat gct aaa ggc gac gct tct gta cgt ttt gct gtt tcg aaa 315
Glu Gly Asp Ala Lys Gly Asp Ala Ser Val Arg Phe Ala Val Ser Lys
45 50 55

tct gtc gat gag gtt aga gga acg gat act cca ccg gag aag gtt ccg 363
Ser Val Asp Glu Val Arg Gly Thr Asp Thr Pro Pro Glu Lys Val Pro
60 65 70

cgt cgt gtc ctg ccg tct gga ttt aag ccg gct gaa tcc gcc gst gat 411
Arg Arg Val Leu Pro Ser Gly Phe Lys Pro Ala Glu Ser Ala Gly Asp
75 80 85 90

gct tcg tcc ctg ttc tcc aat att atg cat aag ttt gta aaa gtc gat 459
Ala Ser Ser Leu Phe Ser Asn Ile Met His Lys Phe Val Lys Val Asp
95 100 105

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Asn	Asp	Ser	Ser	Leu	Cys	Met	Lys	Ala	Asn	Asp	Val	Ile	Pro	Gln	Phe	
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Arg	Ser	Asn	Asn	Gly	Lys	Thr	Gln	Glu	Arg	Asn	His	Ala	Phe	Ser	Phe	
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Ser	Gly	Arg	Ala	Glu	Leu	Arg	Ser	Val	Glu	Asp	Ile	Gly	Val	Asp	Gly	
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gat	gtt	cct	ggc	cca	gaa	aca	cca	ggg	atg	cgt	cca	cgt	gct	tct	cgc	699
Asp	Val	Pro	Gly	Pro	Glu	Thr	Pro	Gly	Met	Arg	Pro	Arg	Ala	Ser	Arg	
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Leu	Lys	Arg	Val	Leu	Glu	Asp	Glu	Met	Thr	Phe	Lys	Glu	Asp	Lys	Val	
		190						195					200			
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Pro	Val	Leu	Asp	Ser	Asn	Lys	Arg	Leu	Lys	Met	Leu	Gln	Asp	Pro	Val	
		205					210					215				
tgt	gga	gag	aag	aaa	gaa	gta	aac	gaa	gga	acc	aaa	ttt	gaa	tgg	ctt	843
Cys	Gly	Glu	Lys	Lys	Glu	Val	Asn	Glu	Gly	Thr	Lys	Phe	Glu	Trp	Leu	
	220					225					230					
gag	tct	tct	cga	atc	agg	gat	gcc	aat	aga	aga	cgt	cct	gat	gat	ccc	891
Glu	Ser	Ser	Arg	Ile	Arg	Asp	Ala	Asn	Arg	Arg	Arg	Pro	Asp	Asp	Pro	
	235				240					245					250	
ctt	tac	gat	aga	aag	acc	tta	cac	ata	cca	cct	gat	gtt	ttc	aag	aaa	939
Leu	Tyr	Asp	Arg	Lys	Thr	Leu	His	Ile	Pro	Pro	Asp	Val	Phe	Lys	Lys	
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Met	Ser	Ala	Ser	Gln	Lys	Gln	Tyr	Trp	Ser	Val	Lys	Ser	Glu	Tyr	Met	
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gac	att	gtg	ctt	ttc	ttt	aaa	gtg	ggg	aaa	ttt	tat	gag	ctg	tat	gag	1035
Asp	Ile	Val	Leu	Phe	Phe	Lys	Val	Gly	Lys	Phe	Tyr	Glu	Leu	Tyr	Glu	
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Leu	Asp	Ala	Glu	Leu	Gly	His	Lys	Glu	Leu	Asp	Trp	Lys	Met	Thr	Met	
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agt	ggc	gtg	gga	aaa	tgc	aga	cag	gtt	ggc	atc	tct	gaa	agt	ggg	ata	1131
Ser	Gly	Val	Gly	Lys	Cys	Arg	Gln	Val	Gly	Ile	Ser	Glu	Ser	Gly	Ile	
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gat	gag	gca	gtg	caa	aag	cta	tta	gct	cgt	gga	tat	aaa	gtt	gga	cga	1179
Asp	Glu	Ala	Val	Gln	Lys	Leu	Leu	Ala	Arg	Gly	Tyr	Lys	Val	Gly	Arg	
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Ile Glu Gln Leu Glu Thr Ser Asp Gln Ala Lys Ala Arg Gly Ala Asn	
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Thr Ile Ile Pro Arg Lys Leu Val Gln Val Leu Thr Pro Ser Thr Ala	
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Ser Glu Gly Asn Ile Gly Pro Asp Ala Val His Leu Leu Ala Ile Lys	
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Glu Ile Lys Met Glu Leu Gln Lys Cys Ser Thr Val Tyr Gly Phe Ala	
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Phe Val Asp Cys Ala Ala Leu Arg Phe Trp Val Gly Ser Ile Ser Asp	
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Asp Ala Ser Cys Ala Ala Leu Gly Ala Leu Leu Met Gln Val Ser Pro	
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Lys Glu Val Leu Tyr Asp Ser Lys Gly Leu Ser Arg Glu Ala Gln Lys	
445 450 455	
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Ala Leu Arg Lys Tyr Thr Leu Thr Gly Ser Thr Ala Val Gln Leu Ala	
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Pro Val Pro Gln Val Met Gly Asp Thr Asp Ala Ala Gly Val Arg Asn	
475 480 485 490	
ata ata gaa tct aac gga tac ttt aaa ggt tct tct gaa tca tgg aac	1659
Ile Ile Glu Ser Asn Gly Tyr Phe Lys Gly Ser Ser Glu Ser Trp Asn	
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Cys Ala Val Asp Gly Leu Asn Glu Cys Asp Val Ala Leu Ser Ala Leu	
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Gly Glu Leu Ile Asn His Leu Ser Arg Leu Lys Leu Glu Asp Val Leu	
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Lys His Gly Asp Ile Phe Pro Tyr Gln Val Tyr Arg Gly Cys Leu Arg	
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Ile Asp Gly Gln Thr Met Val Asn Leu Glu Ile Phe Asn Asn Ser Cys	
555 560 565 570	
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Asp Gly Gly Pro Ser Gly Thr Leu Tyr Lys Tyr Leu Asp Asn Cys Val	
575 580 585	

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Ser Pro Thr Gly Lys Arg Leu Leu Arg Asn Trp Ile Cys His Pro Leu	
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Lys Asp Val Glu Ser Ile Asn Lys Arg Leu Asp Val Val Glu Glu Phe	
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acg gca aac tca gaa agt atg caa atc act ggc cag tat ctc cac aaa	2043
Thr Ala Asn Ser Glu Ser Met Gln Ile Thr Gly Gln Tyr Leu His Lys	
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Leu Pro Asp Leu Glu Arg Leu Leu Gly Arg Ile Lys Ser Ser Val Arg	
635 640 645 650	
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Ser Ser Ala Ser Val Leu Pro Ala Leu Leu Gly Lys Lys Val Leu Lys	
655 660 665	
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Gln Arg Val Lys Ala Phe Gly Gln Ile Val Lys Gly Phe Arg Ser Gly	
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Ile Asp Leu Leu Ala Leu Gln Lys Glu Ser Asn Met Met Ser Leu	
685 690 695	
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Leu Tyr Lys Leu Cys Lys Leu Pro Ile Leu Val Gly Lys Ser Gly Leu	
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Glu Leu Phe Leu Ser Gln Phe Glu Ala Ala Ile Asp Ser Asp Phe Pro	
715 720 725 730	
aat tat cag aac caa gat gtg aca gat gaa aac gct gaa act ctc aca	2379
Asn Tyr Gln Asn Gln Asp Val Thr Asp Glu Asn Ala Glu Thr Leu Thr	
735 740 745	
ata ctt atc gaa ctt ttt atc gaa aga gca act caa tgg tct gag gtc	2427
Ile Leu Ile Glu Leu Phe Ile Glu Arg Ala Thr Gln Trp Ser Glu Val	
750 755 760	
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Ile His Thr Ile Ser Cys Leu Asp Val Leu Arg Ser Phe Ala Ile Ala	
765 770 775	
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Ala Ser Leu Ser Ala Gly Ser Met Ala Arg Pro Val Ile Phe Pro Glu	
780 785 790	
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Ser Glu Ala Thr Asp Gln Asn Gln Lys Thr Lys Gly Pro Ile Leu Lys	
795 800 805 810	
atc caa gga cta tgg cat cca ttt gca gtt gca gcc gat ggt caa ttg	2619
Ile Gln Gly Leu Trp His Pro Phe Ala Val Ala Ala Asp Gly Gln Leu	
815 820 825	

cct gtt ccg aat gat ata ctc ctt ggc gag gct aga aga agc agt ggc	2667
Pro Val Pro Asn Asp Ile Leu Leu Gly Glu Ala Arg Arg Ser Ser Gly	
830 835 840	
agc att cat cct cgg tca ttg tta ctg acg gga cca aac atg ggc gga	2715
Ser Ile His Pro Arg Ser Leu Leu Leu Thr Gly Pro Asn Met Gly Gly	
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Lys Ser Thr Leu Leu Arg Ala Thr Cys Leu Ala Val Ile Phe Ala Gln	
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Leu Gly Cys Tyr Val Pro Cys Glu Ser Cys Glu Ile Ser Leu Val Asp	
875 880 885 890	
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Thr Ile Phe Thr Arg Leu Gly Ala Ser Asp Arg Ile Met Thr Gly Glu	
895 900 905	
agt acc ttt ttg gta gaa tgc act gag aca gcg tca gtt ctt cag aat	2907
Ser Thr Phe Leu Val Glu Cys Thr Glu Thr Ala Ser Val Leu Gln Asn	
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gca act cag gat tca cta gta atc ctt gac gaa ctg ggc aga gga act	2955
Ala Thr Gln Asp Ser Leu Val Ile Leu Asp Glu Leu Gly Arg Gly Thr	
925 930 935	
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Ser Thr Phe Asp Gly Tyr Ala Ile Ala Tyr Ser Val Phe Arg His Leu	
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Val Glu Lys Val Gln Cys Arg Met Leu Phe Ala Thr His Tyr His Pro	
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Leu Thr Lys Glu Phe Ala Ser His Pro Arg Val Thr Ser Lys His Met	
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 690 695 700
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<210> 61
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 <400> 63
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 <210> 64
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<210> 67

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catccgaatg ccattgttc 19

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gaaaaaacgc tactttcgtg g 21

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caagagcaat atcaagagca gc 22

<210> 70

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Arabidopsis thaliana subspecies

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catgcaattt gcatctgagg 20

<210> 71
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Arabidopsis thaliana subspecies

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<210> 72
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<210> 73
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thaliana subspecies

<400> 73
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<210> 74
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Arabidopsis
thaliana subspecies

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tgatgctctc tgaaacaaga gc 22

<210> 76

<211> 21

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<223> Forward primer for PCR amplification of NGA8 SSLP marker in Arabidopsis thaliana subspecies

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<210> 77

<211> 22

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<223> Reverse primer for PCR amplification of NGA8 SSLP marker in Arabidopsis thaliana subspecies

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<210> 78

<211> 21

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<223> Forward primer for PCR amplification of NGA1107 SSLP marker in Arabidopsis thaliana subspecies

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gcgaaaaaac aaaaaaatcc a 21

<210> 79

<211> 21

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<210> 80

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Arabidopsis thaliana subspecies

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<210> 81

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Arabidopsis thaliana subspecies

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tctccccact agtttttgtgt cc 22

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Arabidopsis thaliana subspecies

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taccgtcaat ttcacgccc 19

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Arabidopsis thaliana subspecies

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ggatccctaa ctgtaaaatc cc 22

<210> 84
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aatcccagta accaaacaca ca 22

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<210> 86
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<210> 88

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<210> 90
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Arabidopsis thaliana subspecies

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<400> 91

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<210> 92
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<400> 92

ggagaaaatg tcactctcca cc 22

<210> 93
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<400> 93

aggcatggga gacatttacg 20

<210> 94
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<210> 95
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<210> 96
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Arabidopsis thaliana subspecies

<400> 96

tcaggaggaa ctaaagtgag gg 22

<210> 97

<211> 22

<212> DNA

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<223> Reverse primer for PCR amplification of NGA129 SSLP marker in Arabidopsis thaliana subspecies

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